MOLECULAR CHARACTERIZATION OF THROMBOPHILIA MUTATIONS IN PAKISTANI FEMALES: ROLE OF FACTOR V- LEIDEN IN CAUSING PREECLAMPSIA

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Abstract

The aim of this study is to analyze the prevalence of thrombophilic mutations in Pakistani pregnant females. A total of 2000 pregnant females registered in Gynae unit II, Jinnah Hospital, Allama Igbal medical college with pregnancy induced hypertension during Aug 2016 to Aug 2020 are included in this study. The hypertension of these patients was characterized on basis of disease severity, proteinuria and platelet count etc. After approval from ethical committee and taking informed consent, the total of 100 pregnant females diagnosed with preeclampsia and 100 healthy control pregnant females which fulfill the inclusion criteria of the study were included for mutational analysis. The demographic and medical details of these patients were recorded. The mutational analysis is done by using tetra ARMS PCR. The single nucleotide polymorphism i.e Factor V Leiden G1691A, MTHFR C677T, MTHFR A1298C, FII G20210A was studied in all samples. The prevalence of Factor V Leiden is 60%, MTHFR C677T 69%, FII G20210A 52%, while MTHFR A1298C is 5 % in cases. This is first case control study to identify the role thrombophilia mutations in Pakistani pregnant females affected with preeclampsia. This study confirms the role of hereditary thrombophilia in progression of preeclampsia in pregnant females of Pakistan, the heterozygous form of FV- Leiden and MTHFR C677T and FII G20210A are more prevalent in Pakistani pregnant females presented with preeclampsia, this particular thrombophilia marker can be used for early diagnosis of preeclampsia in clinical practices as genetic risk factors in low socioeconomic background of Pakistan

Keywords: Preeclampsia, Pregnancy induced hypertension, Eclampsia, FV-Leiden, Prothrombin, methylenetetrahydrofolate reductase.

1. INTRODUCTION:

Preeclampsia is distinctive due to occurrence of high blood pressure and albuminuria which happens in women in their 20th week of gestation, without previous history of hypertension (1). Preeclampsia has highest mortality and morbidity rate worldwide; global death rate of pregnant females is 70,000 while 500,000 fetus die annually (2). In developing countries, every year almost 500,000 women die due to obstetric complications, 10-15% of these are caused by preeclampsia (3). The mortality rate due to preeclampsia is equally high in Pakistan where 1 in 89 pregnant female die due to preeclampsia complications (4).

Almost 70 biological candidate genes have been reported to involve in preeclampsia (5) The main areas which have been focused so far for treatment and slow down the evolution of disease genetic and epidemiological factors. The eminence of proteinuria is the area of interest for nephrologists. Few new discoveries also mentioned the role of angiogenic factors in circulation which results endothelial dysfunction. Particularly maternal obesity, hypertension, kidney disease, hyperlipidemia, insulin resistance, and thrombophilia are the risk factors for preeclampsia. The vascular biologists have close interest because the advance research will open role of endothelial function in progression of preeclampsia (6). Preeclampsia is considered as self-limiting disorder that subsides after the removal of placenta. The fetal morbidity is high and also mother suffers long term health defects like high risk of cardiovascular diseases etc. a study in which preeclampsia affected women have examined after three years of pregnancy through Doppler's studies, and have done brachial artery reactivity the results indicated abnormal endothelial dependent flow-mediated arterial dilation. The carriers of these mutations appear asymptomatic during pregnancy so it is difficult to diagnose until symptoms appear. Undiagnosed hereditary thrombophilia causes thrombosis which is the source of preeclampsia. Thrombosis can lead pregnant female towards worse complications of preeclampsia like eclampsia, intrauterine growth retardation and intrauterine death (IUD) (7). The most frequent mutations responsible for hereditary thrombophilia are factor V Leiden (FVL), methylenetetrahydrofolate reductase (MTHFR), and prothrombin (8).

Point mutation in clotting factor V gene causes the FVL mutation in which glutamine (cleavage site of activated protein C) at position 506 of factor V is substituted by arginine (Gln 506 Arg). Due to this mutation, the altered protein resists cleavage by activated protein C which is seen in inherited familial thrombophilia and venous thrombosis patients (9). FVL mutation causes placental abruption, fetal death, severe preeclampsia and intrauterine growth restriction in 20% of the pregnant females (10).

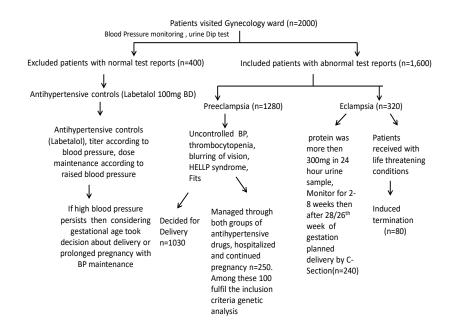
Other common polymorphisms associated with preeclampsia include methylenetetrahydrofolate reductase (MTHFR) gene mutations i.e. C677T and A1298C (11). When methyl-tetrahydrofolate is less available then it will not cause re-methylation of homocysteine, this results in high levels of homocysteine in plasma causing hyperhomocysteinemia (12). These mutations result in increased levels of plasma homocysteine thereby causing homocysteineemia that harms the vascular endothelium. This can enhance thromboembolic threat which causes preeclampsia, placental abruption and still births (13). Mutations in prothrombin (FII), which is a precursor of the serine protease thrombin, are also related to preeclampsia. Prothrombin is a 72 kDa glycoprotein (14) which activates platelet and generates fibrin and clotting factors Va, VIIIa, and XIII (15). A single nucleotide substitution (G>A) at position 20210 in the 3'-untranslated region in the sequence of gene which encodes prothrombin causes increased levels of plasma prothrombin that increases the risk of deep venous thrombosis (16). This effect of inherited thrombophilia causes preeclampsia during pregnancy (17).

The aim of our study was to clarify the association between mutations in thrombophilic factor genes (FVL, MTHFR and prothrombin) and preeclampsia. The genetic makeup of Pakistani people is heterogeneous. Most of the preeclampsia causing genes has been identified in developed countries including US, Canada and Germany but the data of Pakistani population is lacking. Therefore, it is difficult to predict the onset of disease and the pathway of pathogenicity (Khidri et al). The prevalence and association of hereditary thrombophilic mutations with preeclampsia has not been studied in the Pakistani population previously, up to the best of our knowledge. The present research article aims to describe molecular characterization of hereditary thrombophilic mutations in Pakistani pregnant females suffering from preeclampsia. Four SNPs, FVL, MTHFR 677, MTHFR 1298 and prothrombin that are most commonly related to thrombophilia, have been selected for this study. The findings may help clinicians to understand the disease pathogenicity in a better way thereby leading to improved treatment options.

2. MATERIALS AND METHODS

This study is a case control observational study. The subjects included in it were enlisted from August, 2016 to August, 2020 from Gynae Unit II, Jinnah Hospital, Allama Iqbal Medical College, and Lahore, Pakistan. This hospital is good representative of the preeclampsia patients from all the major urban and rural areas all over the Punjab province of Pakistan. The subjects selected for this study was unrelated and 2,000 in numbers. This study was conducted with approval from institutional review and ethical board of institute of Zoology, University of the Punjab, Lahore. The declaration of Helsinki developed by The World Medical Association was completely followed in this project to follow the ethical principles for medical research involving human subjects, including research on identifiable human material and data.

2.1: Flow chart, (Explains the registration of patients in the study period of September 2016 to March 2020)



The 2000 patients visited the gynecological unit II, Jinnah hospital, Allama Igbal medical college, Lahore, Pakistan with suspection of preeclampsia. First step after patient get registered in the unit, their blood pressure was monitored and urine dip test was performed. Those patients who were normal in urine dip test with raised blood pressure (n= 400) were administered antihypertensive drugs (Labetalol 100 mg BD) titer given were according to blood pressure, dose were maintained according to raised blood pressure, if high blood pressure were persistent then gestational age was considered and took decision about delivery through caesarean section or decided to prolong pregnancy for low gestational age subjects with drugs which control blood pressure, the number of these patients were 400. As these patients were with only raised blood pressure and urine dip test was normal. The remaining 1600 patients were abnormal in diagnostic tests, like excretion of proteins in urine 0.3 mgs to 3 gms or 2+ in urine dip test. These patients were included in the list of preeclampsia (n=1280) and admitted to the hospital for further diagnostic investigation and treatment. The complete blood count showed low platelet count (thrombocytopenia), this was also a marker of preeclampsia, patients were having symptoms like blurring of vision, fits, headache, vertigo, HELLP syndrome, those patients who were near the gestational of about 26 to 28 weeks were decided for delivery (n=1030). The patients who were having controlled symptoms with both groups of hypertensive drugs admitted to hospital (n=250), among these 250 patients 100 patients who fulfilled the inclusion criteria (section: 2.2) were selected for molecular analysis. A group of patients (n=320) having protein more than 300 mgs in 24 hours urine sample,

these patients were admitted to hospital for monitoring and characterized as suffering from eclampsia, after the gestational age of 26 to 28 weeks, these patients were planned for delivery through C-section. Patients who were received with life threatening conditions (n=80) were induced for pregnancy termination.

2.2: Inclusion and exclusion criteria:

The inclusion criteria of subjects in this study is followed according to RCOG (Royal college of obstetrician and gynaeclogy) as raised blood pressure (hypertension i.e. raised blood pressure is more then 140/90 mmHg on two proceedings minimum of six hours apart) and after 20th week of pregnancy occur proteinuria i.e. secreted protein in urine has the significant value of 0.3 grams of protein in urine sample collected within 24 hours and if dip stick test performed the value should be more then 1+. These symptoms appear in previously normotensive females after 20th week of pregnancy. Preeclampsia can get worse if these symptoms appear in already suffering hypertensive females having blood pressure more than 160/110 mmHg reading recorded after every 6 hours. Proteinuria more than 5 gms in collected urine after 24 hours or more than 3+ on drip sick test in two urine samples after every 4 hours, if volume of urine is less than 500 after 24 hours, epigastric or right upper quadrant pain, visual disturbances, pulmonary edema, platelet count less than 100,000/mm³, fetal growth restriction, elevated liver enzymes and low platelets (HELLP) syndrome. Eclampsia was defined as the occurrence of convulsions in women with preeclampsia. The patients with chronic hypertension, renal diseases, antiphospholipid syndrome and infectious diseases and molar pregnancy were not included in the study. The women at gestational age of 20th week, not presented with any sign of preeclampsia until get discharged after delivery of baby. Control population was also having healthy pregnancy without any sign and symptoms of preeclampsia also were taken on for age, parity and ethnic group similarity. The gestational age of healthy controls was 20th week of pregnancy. The pregnant females having renal complications, diabetes and any infectious disease were excluded from the study. 100 patients and 100 controls were selected for molecular analysis of preeclampsia. Each subject included in the study duly signed the informed consent.

2.3: Collection of blood samples and screening of subjects and controls selected for Genetic analysis:

The blood sample of patients and controls were collected from median cubital vein by venipuncture. The blood volume collected was 5ml. The blood was poured in 2 different Vacutainer one was containing EDTA, it prevents blood from clotting and the preserved was used for platelet count and genomic DNA extraction. The other Vacutainer contained gel clot activator almost 2 ml blood was poured into it; it is used to separate blood serum. The serum obtained was used for biochemical analysis before experimental protocols samples were first screened for hepatitis B&C and HIV. Only negative samples for Hep B&C and HIV were processed further.

2.4: Biochemical analysis:

The basic laboratory tests have performed for all the registered patients during 2016 to 2020. The females who are at risk of getting preeclampsia have went through evaluation of hepatic enzyme level, complete blood count (specifically platelet count), 24 hour urine collection for total protein measurement, and dip strip test.

2.5: Genetic analysis:

Tetra ARMS were used for genotyping of all selected SNPs (FV-Leiden, MTHFR 677 & 1298, and FII). Primers were used as described in table 1. PCR amplification conditions were optimized, for FV-Leiden PCR conditions were initial denaturation at 95 degree for 5 minutes, 30 cycles of denaturation at 95 degree for 30 seconds, annealing at 50.7 degree for 30 seconds, then extension at 72 degrees for 5 minutes. For MTHFR 677 & 1298 and FII other PCR reaction condition thermo cycler were same except annealing temperature i.e. 54.7, 50.7, 54.0 degrees respectively. The PCR results were analyzed on 2% agarose gel electrophoresis.

2.7: Statistical analysis:

Genotypic and allelic frequencies were calculated and hardy-Weinberg equilibrium was calculated. The chi-square test has applied to the continuous and categorical variables, respectively. A P-value of less than 0.05 was considered as statistically significant. The continuous and categorical data was analyzed by independent sample t-test and chi square tests, respectively (IBM Corp, 2016). (IBM Corp. Released 2016. IBM SPSS Statistics for Windows, Version 24.0. Armonk, NY: IBM Corp. Source: https://www.ibm.com/analytics/spss-statistics-software)

Candidate gene (SNP)	te gene (SNP) rs- Number Primers		Sequence	Product size(bp)
Factor V Leiden		FVL-Common F	5'CAGGAACAACACCATGATCAGAGC'3	501
Nucleotide change: G1691A		FVL-Common R	5'TAATCAACTTGCTCAACACATCCGA'3	319
Protein change:	6025	FVL-G	5'AAGAGCAGATCCCTGGACAGACG'3	228
R506Q		FVL-A	5'CAAGGACAAAATACCTGTATTCGTT'3	
Methylene tetra hydro folate		MTHFR-Common F	5'CCCAGCCACTCACTGTTTTAGTTCAGG'3	407
reductase (MTHFR)		MTHFR-Common R	5'GGTGAGAGTGGGGTGGAGGGAGCTTAT'3	
Nucleotide change: C677T		MTHFR-C	5'CAAAGAAAAGCTGCGTGATGATGAAATAGG'3	273
Protein change: A222V	1801133	MTHFR-T	5'TTGAAGGAGAAGGTGTCTGCGGGCGT'3	190
Methylene tetra hydro folate		MTHFR-Common F	5'GAAGAAGTTTGCATGCTTGTGGTTG'3	593
reductase (MTHFR)		MTHFR-Common R	5'CAGGCAAGTCACCTGGGAGAGA'3	
Nucleotide change: A1298C		MTHFR-C	5'GGCAAAGAACGAAGACTTCAAAGACACATT'3	281
Protein change: E429A	1801131	MTHFR-A	5'GAGGAGCTGACCAGTGATGC'3	361
Prothrombin (FII)		FII-Common F	5'GCCTGAAGAAGTGGATACAGAAGGTCAT'3	245
Nucleotide change: A20210G		FII-Common R	5'CACCAGGTGGTGGATTCTTAAGTCTTCT'3	
Protein change:		FII-A	5'TGGTTCCCAATAAAAGTGACTCTCATCA'3	169
(This mutation, which occurs in a		FII-G	5'GAATAGCACTGGGAGCATTGAGGATC'3	130
region of the gene called the 3'				
untranslated region, causes the gene 179996				
to be overactive and leads to the				
production of too much prothrombin).				

Table 1: candidate genes with nucleotide position, primers sequences and
product size.

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/ Journal of Xi'an Shiyou University, Natural Sciences Edition ISSN: 1673-064X E-Publication: Online Open Access Vol: 66 Issue 02 | 2023 DOI 10.17605/OSF.IO/XSN2Q

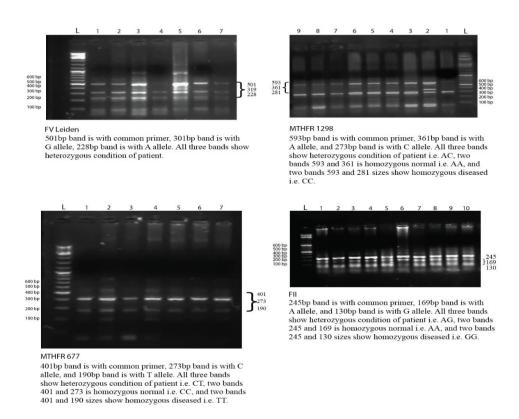


Figure 1: The Figure represents the gel images of tetra ARMS PCR of four mutations FV-Leiden, MTHFR 677, MTHFR 1298 and FII (Prothrombin)

3. RESULTS

The table 2 represented demographic data and clinical characteristics of all participants in the study. The demographic variables like blood group, mode of delivery, pregnancy outcome, proteinuria, gestational age, Hb, SBP (systolic blood pressure) and DBP (diastolic blood pressure) are significantly different between both groups i.e. preeclamptic and control group. The p-value is less than 0.05. The p-value of platelet count is not significantly different between both group (p-value is 0.115)

3.1 Clinical characteristics: comparison between cases and controls:

The comparison of clinical and demographic properties of cases and controls are enlisted in table 2. The blood group, mood of delivery, pregnancy outcome, proteinuria, Hb levels and blood pressure is significantly different between both groups (P<0.001). The platelet count is not significantly associated between cases and controls (p<0.004). The platelet count is not significantly different between both groups (p> 0.115). Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/ Journal of Xi'an Shiyou University, Natural Sciences Edition ISSN: 1673-064X E-Publication: Online Open Access Vol: 66 Issue 02 | 2023 DOI 10.17605/OSF.IO/XSN2Q

Variables		Cases	Controls	p-value
Blood group	A-	7 (7%)	8 (%)	<0.001
	A+	29 (29%)	44 (44%)	
	AB+	11 (11%)	0 (0%)	
	В-	4 (4%)	10 (10%)	
	B+	30 (30%)	19 (19%)	
	0-	0 (0%)	19 (19%)	
	0+	19 (19%)	0 (0%)	
Delivery	LASC	3 (3%)	0 (0%)	<0.001
-	LSCS	63 (63%)	26 (26%)	
	MISSCARRIAGE	20 (20%)	0 (0%)	
	SVD	14 (14%)	74 (74%)	
Pregnancy	Abort	21 (21%)	6 (6%)	0.001
outcome	Alive	76 (76%)	94 (94%)	
	IUD	3 (3%)	0 (0%)	
Proteinuria	0	13 (13%)	92 (92%)	<0.001
	1+	22 (22%)	8 (8%)	
	2+	29 (29%)	0 (0%)	
	3+	35 (35%)	0 (0%)	
	4+	1 (1%)	0 (0%)	
Gestational age		35 ± 3	36.5 ± 4.5	0.004
Hb		10.8 ± 1.5	9.8 ± 1.13	<0.001
SBP		147.7 ± 22	117 ± 11.7	<0.001
DBP		97.7 ± 16.1	77.7 ± 9.6	<0.001
PC		259.1 ± 87.8	276 ± 61.1	0.115

Table 2. Clinical characteristics of participants

3.2 Comparison of demographic and clinical characters among cases:

Table 1-4 (tables provided in supplementary data) explains the distribution of clinical and demographic characteristics association with all four SNPs. Heterozygous Factor V Leiden (SNP1) and wild type has no significant correlation with any of clinical and demographic characters. The blood group, mood of delivery, pregnancy outcome, proteinuria, gestational age, hemoglobin level, systolic and diastolic blood pressure and platelet count has P values 0.538, 0.425, 0.580, 0.565, 0.946, 0.791, 0.414, 0.150, 0.568 respectively. Heterozygous MTHFR 677 (SNP 2) and wild type has no significant correlation with any of clinical and demographic characters. The blood group, mood of delivery, pregnancy outcome, proteinuria, gestational age, hemoglobin level, systolic and diastolic blood pressure and platelet count has P values 0.538, 0.157, 0.129, 0.900, 0.151, 0.905, 0.134, 0.090, 0.892 respectively. Heterozygous MTHFR 1298 (SNP 3) and wild type has no significant correlation with any of clinical and demographic characters. The blood group, mood of delivery, pregnancy outcome, proteinuria, gestational age, hemoglobin level, systolic and diastolic blood pressure and platelet count has P values 0.218, 0.768, 0.918, 0.766, 0.861, 0.877, 0.388, 0.966, 0.431 respectively. Heterozygous FII Prothrombin (SNP 4) and wild type has no significant correlation with any of clinical and demographic characters. The blood group, mood of delivery, pregnancy outcome, proteinuria, gestational age, hemoglobin level, systolic and diastolic blood pressure and platelet count has P values 0.538, 0.035, 0.492, 0.712, 0.335, 0.712, 0.783, 0.383, 0.659 respectively.

3.3 The distribution of allelic and genotypic frequencies of thrombophilic mutations in pregnant Pakistani females:

This case control study is in complete equilibrium with hardy Weinberg principle with respect to distribution of allelic and genotypic frequencies among patients and controls. Table 3 presents the frequency, chi square, odd ratios and p-values of analysis between cases and controls.

The factor V Leiden SNP in cases and controls is highly statistically significant (χ 2= 50, p-value 0.001, OR 0.091), it is highly associated with preeclampsia in heterozygous form. The FII (Prothrombin) SNP in cases and controls is highly statistically significant (χ 2= 28.87, p-value 0.001, OR 0.176), it is highly associated with preeclampsia in heterozygous form. The MTHFR677 in cases and controls is highly statistically significant (χ 2= 37.07, p-value 0.001, OR 0.158), it is highly associated with preeclampsia in heterozygous form. The MTHFR 1298 SNP in cases and controls is not statistically significant (χ 2= 1.33, p-value 0.248, OR 0.388), in this study this SNP is not associated with preeclampsia.

Factor V leiden Genotype (FV)	Subject Types	Frequency	Chi square value	OR (CI)	P value	
GG (wild type)	Cases	40				
GG (Wild type)	Control	88	50.00	0.091	0.001	
GA(Heterozygous)	Cases	60	50.00	(0.044-0.187)	0.001	
GA(Heterozygous)	Control	12				
FII(Prothrombin) Genotype (FII)	Types	Frequency	Chi square value	OR (CI)	P value	
GG (wild type)	Cases	48				
GG (Wild type)	Control	84	20.07	0.176 (0.091-0.341)	0.001	
GA(Heterozygous)	Cases	52	28.87		0.001	
GA(Heterozygous)	Control	16				
MTHFR 677 Genotype (677)	Types	Frequency	Chi square value	OR (CI)	P value	
CC(wild type)	Cases	31				
CC(wild type)	Control	74	07.07	0.158	0.001	
CT(Heterozygous)	Cases	69	37.07	(0.085-0.292)	0.001	
CT(Heterozygous)	Control	26				
MTHFR 1298 Genotype (1298)	Types	Frequency	Chi square value	OR (CI)	P value	
AA(wild type)	Cases	95				
AA(wild type)	Control	98	1.33	0.388 (0.073-2.047)	0.248	
AC(Heterozygous)	Cases	5	1.33		0.240	
AC(Heterozygous)	Control	2				

Table 3: Genotype and allelic frequencies:

4. DISCUSSION

Preeclampsia is a very complicated clinical condition during pregnancy which involves many pathogenic genes which have related to pathophysiology of placenta. The epidemiological research proved genetic basis of preeclampsia. The work on pathological diagnostics identified various candidate genes in the groups like, thrombophilia, immunogenetics, vasoactive proteins, oxidative stress, lipid metabolism and endothelial dysfunction. The research on preeclampsia genetics is still in formative years (5). The familial tendency of preeclampsia has been over and over again verified by epidemiological research. The target of candidate gene and familial study is the discovery of susceptibility locus in genetic clusters for treatment and preventive measures (18).

The inherited thrombophilia is caused by single nucleotide polymorphism in Factor V, which is designated as FV-leiden, the genetic variation, SNP at position 20210 G>A, in prothrombin gene which effects functions performed by this gene and SNPs in MTHFR gene at position 677 C>T and 1298A>C. These mutations if act coordinated then it will increase the risk of thrombotic events which in parallel enhance the effect of these variables in preeclampsia progression. Many epidemiological studies have performed to inspect the role of FV-Leiden, FII (prothrombin), MTHFR (at position 1298 & 677) in causing preeclampsia. A study in case control group in Japan also reported the significant association of MTHFR C677T in causing preeclampsia (19). Another study on Italian population also confirmed the association MTHFR 677 C>T and factor V Leiden with preeclampsia(20). Another case control study in Hungary found significant association of Factor V Leiden mutation frequency higher in preeclampsia women then control population (21).

A study on German/Croatians and Indonesians the mutation of factor V Leiden is significantly associated with preeclampsia (22). A Meta-analysis also discussed the significant association of Factor V Leiden with higher risk of preeclampsia (23). The interaction of Factor V Leiden, FII and MTHFR single nucleotide polymorphism association is also reported in Brazilian population (24). A study on the population of Caucasians and East Asia populations also observed a significant association between MTHFR 677 C>T and risk of preeclampsia (25). The Iranian population expressed the association of MTHFR 1298 SNP with preeclampsia but not MTHFR 677, Factor V Leiden G1691A and FII (Prothrombin G20210A) results were observed similar in cases and controls (26).

This is a case control study, in which Factor V Leiden has a high prevalence i.e. 60%, Methylenetetrahydrofolate reductase (MTHFR C677T) 69%, FII (prothrombin) G20210A 52% while MTHFR A1298C in heterozygous form is 5 % which is less prevalent in cases. In this study the pregnant females have rigorous obstetrical complications related with complications in the maternal fetal flow. In previous studies on preeclampsia genetics it is believed that hereditary thrombophilia factors play a role in the development of preeclampsia. The group of patients belongs to all ethnic group of Pakistan and this analysis provided a clear evidence of sturdy association of preeclampsia with

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/ Journal of Xi'an Shiyou University, Natural Sciences Edition ISSN: 1673-064X E-Publication: Online Open Access Vol: 66 Issue 02 | 2023 DOI 10.17605/OSF.IO/XSN2Q

thrombophilia factors. The criteria of preeclampsia diagnosis were in stringent agreement with the Royal College of obstetricians and gynecologist. All the subjects included in this study no history of chronic hypertension and thromboembolic disorders so that provide a homogenous populace for data analysis in accordance with severe preeclampsia. Gestational hypertension, chronic hypertension, preeclampsia and eclampsia are result in imprecise detection of thrombophilia defects and inclusion of predisposition towards healthy subjects. This study proves that preeclampsia is linked with mutations in thrombophilic factors. Thus these results focus on need to make a difference between real pathology of preeclampsia in comparison with maternal and fetal mortality and morbidity (27). In adding together, the narrow sample size of the involvement of thrombophilia with preeclampsia bring down their statistical significance and this result in its more than assessment or underestimation (28). The sample size in our study is strength of this analysis. This study is in harmony with results reported previously (29). It is the first data on maternal and perinatal consequence on preeclampsia subjects as carrier of thrombophilia. The results express that thrombophilia play a role in causing preeclampsia. Females with Preeclampsia (which results as a consequence of thrombophilia) are more on threat with complications like acute renal failure and placental abruption.

The thrombophilia mutations cause early onset of preeclampsia usually before 28 weeks of gestational age and it cause perinatal complications in pregnant females which leads eventually towards severe preeclampsia ultimately cause delivery before 28th week of gestation, fetal growth restriction and fetal mortality is very high. It shows the direct effect of thrombophilia mutations on fetus and placenta and cause greater severity of preeclampsia.

5. CONCLUSIONS

The results of our study reveal a statistically significant association between thrombophilia mutations and preeclampsia in Pakistani pregnant women. Thrombophilia mutations like Factor V Leiden G1691A, MTHFR 677 & 1298, FII (prothrombin) single nucleotide polymorphism was found significantly associated with preeclampsia in present study. The life threatening complications in mothers suffering from preeclampsia can be extended due to thrombophilia mutations. As a result of this study we suggest to consider these findings during preconception counseling and risk of sever perinatal outcomes. To prevent the recurrence of preeclampsia randomized trials of antithrombotic interventions are suggested

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SUPPLEMENTARY DATA

Supplementary Table 1: Characteristics of preeclampsia patients by SNP1 status

		SNP1						
Characteristics		Cases with heterozygous SNP1		Cas	ses with wild type SNP1	p-value		
		N	Percentage/m ean±SD	N	Percentage/mean ±SD	p-value		
	A-	3	4.8%	4	10.5%			
	A+	19	30.6%	10	26.3%			
Blood group	AB+	8	12.9%	3	7.9%	0.538		
	В-	2	3.2%	2	5.3%	0.556		
	B+	16	25.8%	14	36.8%			
	O+	14	22.6%	5	13.2%			
	LASC	3	4.8%	0	0%			
Delivery	LSCS	40	64.5%	23	60.5%	0.425		
	MISSCARRIAGE	12	19.4%	8	21.1%	0.425		
	SVD	7	11.3%	7	18.4%			
Prognanov	Abort	13	21%	8	21.1%			
Pregnancy outcome	Alive	48	77.4%	28	73.7%	0.580		
outcome	IUD	1	1.6%	2	5.3%			
	0	10	16.1%	3	7.9%			
	1+	13	21%	9	23.7%			
Proteinuria	2+	19	30.6%	10	26.3%	0.565		
	3+	19	30.6%	16	42.1%			
	4+	1	1.6%	0	0%			
Gestational age	-	62	35±3.1	38	34.9±2.8	0.946		
Hb	-	62	10.9±1.6	38	10.8±1.4	0.791		
SBP	-	62	146.2±19.1	38	150±25.9	0.414		
DBP	-	62	99.5±17.9	38	94.7±12.2	0.150		
PC	-	62	263.1±93.5	38	252.6±78.6	0.568		

Supplementary Table 2: Characteristics of preeclampsia patients by SNP2 status:

			SNP2				
		Cases with		Cases with wild type			
Characteristics		he	eterozygous	SNP 2		p-value	
		N	Percentage/	N	Percentage/m	p-value	
		IN	mean±SD	IN	ean±SD		
	A-	3	4.8%	4	10.5%		
	A+	19	30.6%	10	26.3%		
Blood group	AB+	8	12.9%	3	7.9%	0.538	
	B-	2	3.2%	2	5.3%	0.556	
	B+	16	25.8%	14	36.8%		
	O+	14	22.6%	5	13.2%		
	LASC	3	4.4%	0	0%		
Delivery	LSCS	44	64.7%	19	59.4%	0.157	
	MISSCARRIAGE	10	14.7%	10	31.2%	0.157	
	SVD	11	16.2%	3	9.4%		
Pregnancy	Abort	11	16.2%	10	31.2%	0.129	
outcome	Alive	54	79.4%	22	68.8%	0.129	

	IUD	3	4.4%	0	0%	
	0	5	15.6%	8	11.8%	
	1+	7	21.9%	15	22.1%	
Proteinuria	2+	8	25%	21	30.9%	0.900
	3+	12	37.5%	23	33.8%	
	4+	0	0%	1	1.5%	
Gestational age	-	68	35.2±2.9	32	34.3±3	0.151
Hb	-	68	10.8±1.5	32	10.8±1.4	0.905
SBP	-	68	145.4±20.7	32	152±24	0.134
DBP	-	68	95.9±12.7	32	101.6±21.3	0.099
PC	-	68	95.8±12.7	32	101.5±21.3	0.892

Supplementary Table 3: Characteristics of preeclampsia patients by SNP3 status

		SNP3						
		C	ases with		Cases with wild type			
Characteristics		heterozygous		SNP 3		p-value		
		N	Percentage/ mean±SD	Ν	Percentage/ mean±SD	pvalue		
	A-	0	0%	7	7.4%			
	A+	1	20%	28	29.5%			
Blood group	AB+	0	0%	11	11.6%	0.218		
	В-	1	20%	3	3.2%	0.210		
	B+	3	60%	27	28.4%			
	0+	0	0%	19	20%			
Delivery	LASC LSCS MISSCARRIA GE SVD	0 4 1 0	0% 80% 20% 0%	3 59 19 14	3.2% 62.1% 20% 14.7%	0.768		
Pregnancy	Abort	1	20%	20	21.1%			
outcome	Alive	4	80%	72	75.8%	0.918		
outcome	IUD	0	0%	3	3.2%			
	0	0	0%	13	13.7%			
	1+	1	20%	22	22.1%			
Protenuria	2+	1	20%	29	29.5%	0.766		
	3+	3	60%	35	33.7%			
	4+	0	0%	1	1.1%			
Gestational age	-	5	35.2±3	95	34.9±2.9	0.861		
Hb	-	5	10.7±1.4	95	10.8±1.5	0.877		
SBP	-	5	156±35.8	95	147.2±21.1	0.388		
DBP	-	5	98±21.7	95	97.7±15.8	0.966		
PC	-	5	289.4±52	95	257.5±89.2	0.431		

			•	• •	•		
		SNP4					
			ases with	Cases with wild type			
Characteristics		heterozygous		SNP 4		p-value	
		Ν	Percentage/ mean±SD	N	Percentage/ mean±SD	p-value	
	A-	3	4.8%	4	10.5%		
	A+	19	30.6%	10	26.3%		
Blood group	AB+	8	12.9%	3	7.9%	0.538	
	В-	2	3.2%	2	5.3%	0.550	
	B+	16	25.8%	14	36.8%		
	0+	14	22.6%	5	13.2%		
	LASC	3	5.8%	0	0%		
Delivery	LSCS	34	65.4%	29	60.4%	0.035	
	MISSCARRIAGE	12	23.1%	8	16.7%	0.000	
	SVD	3	5.8%	11	22.9%		
Pregnancy	Abort	13	25%	8	16.7%		
outcome	Alive	37	71.2%	39	81.2%	0.492	
	IUD	2	3.8%	1	2.1%		
	0	6	11.5%	7	14.6%		
	1+	12	23.1%	10	20.8%		
Proteinuria	2+	13	25%	16	33.3%	0.712	
	3+	20	38.5%	15	31.2%		
	4+	1	1.9%	0	0%		
Gestational age	-	52	34.7±3.4	48	35.2±2.5	0.335	
Hb	-	52	10.8±1.5	48	10.9±1.6	0.712	
SBP	-	52	147.1±22.5	48	148.3±21.4	0.783	
DBP	-	52	96.3±13.1	48	99.1±18.7	0.383	
PC	-	52	262.8±100	48	255±73	0.659	

Supplementary Table 4: Characteristics of preeclampsia patients by SNP4 status